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UniProtKB/TrEMBL entry Q9XEI0



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Entry information

Entry name	Q9XEI0_STERE
Primary accession number	Q9XEI0
Secondary accession numbers	None
Integrated into TrEMBL on	November 1, 1999
Sequence was last modified on	November 1, 1999 (Sequence version 1)
Annotations were last modified on	April 18, 2006 (Entry version 23)

Name and origin of the protein

Protein name	Kaurene synthase
Synonyms	None
Gene name	Name: KS22-1
From	<i>Stevia rebaudiana</i> (Stevia) [TaxID: 55670]
Taxonomy	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanu Asterales; Asteraceae; Asteroideae; Eupatorieae; Stevia

References

[1] NUCLEOTIDE SEQUENCE.

TISSUE=Leaf;

PubMed=10504563 [NCBI, ExPASy, EBI, Israel, Japan]

Richman A.S., Gijzen M., Starratt A.N., Yang Z., Brandle J.E.;

"Diterpene synthesis in *Stevia rebaudiana*: recruitment and up-regulation of key enzymes the gibberellin biosynthetic pathway.";

Plant J. 19:411-421(1999).

Comments

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Cross-references

Sequence databases

EMBL AF097311; AAD34295.1; -; mRNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

3D structure databases

HSSP Q40577; 1HX9. [HSSP ENTRY / PDB]

ModBase Q9XEI0.

2D gel databases

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Ontologies

GO GO:0016829; Molecular function: lyase activity (*inferred from electronic annotation*)
 GO GO:0008152; Biological process: metabolism (*inferred from electronic annotation*)
 QuickGo view.

Family and domain databases

InterPro IPR008930; Terp_cyc_toroid.
 IPR001906; Terp_synth-like.
 IPR008949; Terpenoid_synth.
 IPR005630; Tps_metal_bd.
 Graphical view of domain structure.
 Pfam PF01397; Terpene_synth; 1.
 PF03936; Terpene_synth_C; 1.
 Pfam graphical view of domain structure.
 ProDom [Domain structure / List of seq. sharing at least 1 domain]

Other

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

None

Features

None

Sequence information

Length: **784** Molecular weight: **89401 Da** CRC64: **284BD3972DC09051** [This is a checksum or sequence]

```

      10      20      30      40      50      60
MNLSLCIASP LLTKSNRPAA LSAIHTASTS HGGQTNPTNL IIDTTKERIQ KQFKNVEISV

      70      80      90     100     110     120
SSYDTAWVAM VPSPNSPKSP CFPECLNWL I NNQLNDGSWG LVNHTHNHNH PLLKDSLST

     130     140     150     160     170     180
LACIVALKRW NVGEDQINKG LSFIESNLAS ATEKSQPSPI GFDIIFPGLL EYAKNLDINL

     190     200     210     220     230     240
LSKQTDfSLM LHKRELEQKR CHSNEMDGYL AYISEGLGNL YDWNMVKKYQ MKNGSVFNSP

     250     260     270     280     290     300
SATAAAFINH QNPGCLNYLN SLLDKFGNAV PTVYPHDLFI RLSMVDTIER LGISHHFRVE

     310     320     330     340     350     360
IKNVLDETYR CWVERDEQIF MDVVTCALAF RLLRINGYEV SPDPLAEITN ELALKDEYAA

     370     380     390     400     410     420

```

```

LETYHASHIL YQEDLSSGKQ ILKSADFLKE IISTDSNRLS KLIHKEVENA LKFPINTGLE
      430      440      450      460      470      480
RINTRRNIQL YNVDNTRILK TTYHSSNISN TDYLRLAVED FYTCQSIYRE ELKGLERWVV
      490      500      510      520      530      540
ENKLDQLKFA RQKTAYCYFS VAATLSSPEL SDARISWAKN GILTTVVDDF FDIGGTIDEL
      550      560      570      580      590      600
TNLIQCVEKW NVDVDKDCCS EHVRIFLAL KDAICWIGDE AFKWQARDVT SHVIQTWLEL
      610      620      630      640      650      660
MNSMLREAIW TRDAYVPTLN EYMENAYVSF ALGPIVKPAI YFVGPKLSEE IVESSEYHNL
      670      680      690      700      710      720
FKLMSTQGRL LNDIHSFKRE FKEGKLNAVA LHLSNGESGK VEEVVVEEMM MMIKNKRKEL
      730      740      750      760      770      780
MKLIFEENGs IVPRACKDAF WNMCHVLNFF YANDDGFTGN TILDTVKDII YNPLVLVNEN

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or at NCBI (USA)Sequence analysis tools: ProtParam,
ProtScale, Compute pI/Mw, PeptideMass,
PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

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NiceZyme View of ENZYME: EC 2.5.1.21

Official Name	
Squalene synthase.	
Alternative Name(s)	
Farnesyl-diphosphate farnesyltransferase.	
Farnesyltransferase.	
Presqualene synthase.	
Presqualene-diphosphate synthase.	
Squalene synthetase.	
Reaction catalysed	
1. 2 farnesyl diphosphate <=> diphosphate + presqualene diphosphate	
2. Presqualene diphosphate + NAD(P)H <=> squalene + diphosphate + NAD(P)(+)	
Cofactor(s)	
Magnesium or manganese.	
Comment(s)	
In the absence of NAD(P)H, presqualene diphosphate is accumulated.	
Cross-references	
Biochemical	
Pathways; map number(s)	E10
PROSITE	PDOC00802
BRENDA	2.5.1.21
PUMA2	2.5.1.21
PRIAM enzyme-specific profiles	2.5.1.21
Kyoto University	
LIGAND chemical database	2.5.1.21
IUBMB Enzyme Nomenclature	2.5.1.21
IntEnz	2.5.1.21
MEDLINE	Find literature relating to 2.5.1.21
MetaCyc	2.5.1.21
P53799, FDFT_ARATH; Q752X9, FDFT_ASHGO; P78589, FDFT_CANAL; Q9HGZ6, FDFT_CANGA; P37268, FDFT_HUMAN; P53798, FDFT_MOUSE;	

UniProtKB/Swiss-Prot	Q7S4Z6, FDFT_NEUCR;	P53800, FDFT_NICBE;	O74165, FDFT_PICJA;
	Q02769, FDFT_RAT;	P36596, FDFT_SCHPO;	Q92459, FDFT_USTMA;
	Q9Y753, FDFT_YARLI;	P29704, FDFT_YEAST;	

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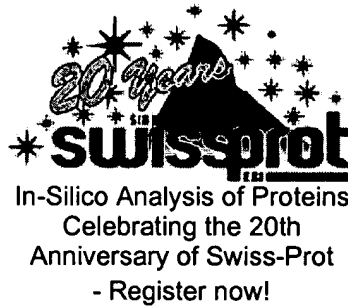
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Entry information

Entry name	GGPPS_YEAST
Primary accession number	Q12051
Secondary accession numbers	None
Integrated into Swiss-Prot on	March 21, 2006
Sequence was last modified on	November 1, 1996 (Sequence version 1)
Annotations were last modified on	June 13, 2006 (Entry version 33)
Name and origin of the protein	
Protein name	Geranylgeranyl pyrophosphate synthetase
Synonyms	GGPP synthetase GGPPSase Geranylgeranyl diphosphate synthase BET2 suppressor protein 1 Dimethylallyltranstransferase (EC 2.5.1.1)
Includes	Geranyltranstransferase (EC 2.5.1.10) Farnesyltranstransferase (EC 2.5.1.29)
Gene name	Name: BTS1 OrderedLocusNames: YPL069C
From	<i>Saccharomyces cerevisiae</i> (Baker's yeast) [TaxID: 4932]
Taxonomy	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.


References

- [1] NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND FUNCTION.
DOI=10.1074/jbc.270.37.21958; PubMed=7665600 [NCBI, ExPASy, EBI, Israel, Japan]
Jiang Y., Proteau P., Poulter D., Ferro-Novick S.;
"BTS1 encodes a geranylgeranyl diphosphate synthase in *Saccharomyces cerevisiae*.";
J. Biol. Chem. 270:21793-21799(1995).

[2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=S288c / AB972;

PubMed=9169875 [NCBI, ExPASy, EBI, Israel, Japan]

Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Apari A., Barrell B.G., Badcock K., Benes V., Botstein D., Bowman S., Brueckner M., Carpenter Cherry J.M., Chung E., Churcher C.M., Coster F., , Hani J.;

"The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XVI.";

Nature 387:103-105(1997).

[3] NUCLEOTIDE SEQUENCE [GENOMIC DNA].

STRAIN=S288c;

Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E., Hu Y., Vannberg Weger J., Kramer J., Moreira D., Kelley F., Zuo D., Raphael J., Hogle C., Jepson D.,

Williamson J., Camargo A., Gonzaga L., , LaBaer J.;

"Creation of the YFLEX clone resource: cloning of *Saccharomyces cerevisiae* ORFs in the Gateway recombinational cloning system.";

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

[4] LEVEL OF PROTEIN EXPRESSION.

DOI=10.1038/nature02046; PubMed=14562106 [NCBI, ExPASy, EBI, Israel, Japan]

Ghaemmaghami S., Huh W.-K., Bower K., Howson R.W., Belle A., Dephoure N., O'Shea J. Weissman J.S.;

"Global analysis of protein expression in yeast.";

Nature 425:737-741(2003).

[5] FUNCTION.

DOI=10.1111/j.1600-0854.2004.00213.x; PubMed=15296494 [NCBI, ExPASy, EBI, Israel Japan]

Shiflett S.L., Vaughn M.B., Huynh D., Kaplan J., Ward D.M.;

"Bph1p, the *Saccharomyces cerevisiae* homologue of CHS1/beige, functions in cell wall formation and protein sorting.";

Traffic 5:700-710(2004).

Comments

- **FUNCTION:** Catalyzes the trans-addition of the 3 molecules of IPP onto DMAPP to form geranylgeranyl pyrophosphate. Required for the membrane attachment of YPT1 and Sfi1. May be involved in vesicle trafficking and protein sorting.
- **CATALYTIC ACTIVITY:** Dimethylallyl diphosphate + isopentenyl diphosphate = dimethylallyl diphosphate + geranyl diphosphate.
- **CATALYTIC ACTIVITY:** Geranyl diphosphate + isopentenyl diphosphate = dimethylallyl diphosphate + trans,trans-farnesyl diphosphate.
- **CATALYTIC ACTIVITY:** Trans,trans-farnesyl diphosphate + isopentenyl diphosphate = dimethylallyl diphosphate + geranylgeranyl diphosphate.
- **PATHWAY:** Isoprenoid biosynthesis.
- **SUBCELLULAR LOCATION:** Cytoplasm (*By similarity*).
- **MISCELLANEOUS:** Present with 2840 molecules/cell.
- **SIMILARITY:** Belongs to the FPP/GGPP synthetase family.

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Cross-references

Sequence databases

U39205; AAB68296.1; -;

Genomic_DNA.

U31632; AAA83262.1; -;

[EMBL / GenBank / DDBJ]

[CoDingSequence]

[EMBL / GenBank / DDBJ]

EMBL	Genomic_DNA. AY692852; AAT92871.1; -; Genomic_DNA.	[CoDingSequence] [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	S60921; S60921.	

3D structure databases

ModBase Q12051.

Protein-protein interaction databases

IntAct Q12051; -.

DIP Q12051.

2D gel databases

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Organism-specific gene databases

SGD S000005990; BTS1.

Yeast-GFP YPL069C.

Ontologies

	GO:0005739; Cellular component: mitochondrion (<i>inferred from direct assay</i>).
	GO:0004311; Molecular function: farnesyltransferase activity (<i>inferred from direct assay</i>).
GO	GO:0016114; Biological process: terpenoid biosynthesis (<i>inferred from direct assay</i>).
	QuickGo view.

Family and domain databases

InterPro	IPR000092; Polyprenyl_synt. IPR008949; Terpenoid_synt. Graphical view of domain structure.
Pfam	PF00348; polyprenyl_synt; 1. Pfam graphical view of domain structure.
PROSITE	PS00723; POLYPRENYL_SYNTHET_1; 1. PS00444; POLYPRENYL_SYNTHET_2; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
BLOCKS	Q12051.

Genome annotation databases

Ensembl YPL069C; Saccharomyces cerevisiae. [Contig view]
GenomeReviews U00094_GR; YPL069C.

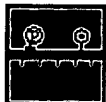
Other

LinkHub	Q12051; -.
ProtoNet	Q12051.
UniRef	View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Carotenoid biosynthesis; Complete proteome; Isoprene biosynthesis; Multifunctional enzyme; Protein transport; Transferase; Transport.

Features



Feature table viewer

Key	From	To	Length	Description	FTId
CHAIN	1	335	335	Geranylgeranyl pyrophosphate synthetase.	PRO_0000228
ACT_SITE	169	169		By similarity.	

Sequence information

Length: **335 AA** [This is the length of the unprocessed precursor] Molecular weight: **38651 Da** [This is the MW of the unprocessed precursor] CRC64: **4C7D6527FF29F157** is a checksum on the sequence

<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>
MEAKIDELIN	NDPVWSSQNE	SLISKPYNHI	LLKPGKNFRL	NLIVQINRVM	NLPKDQLAIV
<u>70</u>	<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>	<u>120</u>
SQIVELLHNS	SLLIDDIEDN	APLRRGQTTS	HLIFGVPSTI	NTANYMYFRA	MQLVSQLTTK
<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>
EPLYHNLITI	FNEELINLHR	GQGLDIYWRD	FLPEIIPTQE	MYLNMVMNKT	GGLFRLTLRL
<u>190</u>	<u>200</u>	<u>210</u>	<u>220</u>	<u>230</u>	<u>240</u>
MEALSPSSH	GHSLVPFINL	LGIIYQIRDD	YLNKDFQMS	SEKGFAEDIT	EGKLSFPIVH
<u>250</u>	<u>260</u>	<u>270</u>	<u>280</u>	<u>290</u>	<u>300</u>
ALNFTKTKGQ	TEQHNEILRI	LLLRTSDKDI	KLKLIQILEF	DTNSLAYTKN	FINQLVNMIK
<u>310</u>	<u>320</u>	<u>330</u>			
NDNENKYLPD	LASHSDTATN	LHDELLYIID	HLSEL		

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or at NCBI (USA)



Sequence analysis tools: ProtParam,
ProtScale, Compute pI/Mw, PeptideMass,
PeptideCutter, Dotlet (Java)



ScanProsite, MotifScan



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NPSA Sequence
analysis tools



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